

Additional File 3. Gene loci under positive selection based on the branch-site specific test (Test 2).

Clade 1				
Gene Locus_tag	Locus	Annotation	LRT p-value	FDR p-value
CT852	<i>yhgN</i>	Yhgn Family Protein/putative integral membrane protein	0.000141547	0.01888237
CT868	-	hypothetical protein	2.45E-05	0.005447167
CT115	-	inclusion membrane protein D	1.07E-06	0.000356845
CT147	-	Hypothetical protein/putative integral membrane protein	0.000174239	0.01936957
CT249	-	hypothetical protein	0.000668414	0.07810895
CT456	-	hypothetical protein /Translocated actin-recruiting phosphoprotein	9.45E-09	6.30E-06
CT619	-	hypothetical protein	4.92E-05	0.0082041
Clade 2				
Gene Locus_tag	Locus	Annotation	LRT -p-value	FDR-p-value
CT011	-	hypothetical protein	3.28E-06	0.002523685
CT308	<i>atpA</i>	V-type ATP synthase subunit A	0.000333876	0.07953066
CT341	<i>dnaJ</i>	heat shock protein J /chaperone protein DnaJ	0.000388903	0.07953066
CT380	<i>phnP</i>	metal-dependent hydrolase	6.17E-06	0.002523685
Clade 3				
Gene Locus_tag	Locus	Annotation	LRT -p-value	FDR-p-value
CT823	<i>htrA</i>	DO Serine protease	0.000103724	0.007713294
CT827	<i>nrdA</i>	ribonucleotide-diphosphate reductase subunit alpha	0.00169824	0.07717557
CT870	<i>pmpF</i>	polymorphic outer membrane protein	0.000673141	0.03670862
CT012	-	hypothetical protein	5.19E-26	2.12E-23
CT065	-	ADP,ATP carrier protein	6.31E-05	0.005162782
CT082	-	hypothetical protein	2.98E-06	0.000305145
CT115	-	inclusion membrane protein D	0.001202199	0.06146242
CT147	-	Hypothetical protein/putative integral membrane protein	3.59E-17	7.34E-15
CT209	<i>leuS</i>	leucyl-tRNA synthetase	0.000150662	0.01027013
CT227	-	hypothetical protein	1.20E-09	1.63E-07
CT244	-	hypothetical protein	9.54E-11	1.56E-08
CT254	-	hypothetical protein/inner membrane protein	0.00042992	0.02705189
CT315	<i>rpoB</i>	DNA-directed RNA polymerase subunit beta	0.001389792	0.06687352
CT375	-	putative oxidoreductase	0.00054153	0.03164082
CT402	<i>ipxK</i>	tetraacyldisaccharide 4'-kinase	2.49E-26	2.04E-23
CT448	<i>secD/secF</i>	bifunctional preprotein translocase	2.14E-07	2.50E-05

CT448	<i>secD/secF</i>	bifunctional preprotein translocase subunit SecD/SecF	2.14E-07	2.50E-05
CT591	<i>sdhB</i>	succinate dehydrogenase iron-sulfur subunit	1.80E-05	0.001632655
CT604	<i>GroEL_2</i>	HSP 60/60 kDa chaperonin GroEL2	4.95E-18	1.35E-15

Clade 4

Gene Locus_tag	Locus	Annotation	LRT p-value	FDR p-value
CT707	<i>tig</i>	trigger factor	0.001668657	0.04300546
CT739	<i>ftsK</i>	cell division protein FtsK	0.000938103	0.0316283
CT745	<i>hemG</i>	protoporphyrinogen oxidase	1.31E-09	8.32E-07
CT748	<i>mfd</i>	transcription-repair coupling factor	0.000859936	0.0316283
CT756	<i>murF</i>	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	0.001175782	0.03354957
CT762	<i>murC/ddlA</i>	bifunctional D-alanyl-alanine synthetase A/UDP-N-acetylmuramate-L-alanine ligase	0.005000301	0.09987443
CT768	-	hypothetical protein	0.000459232	0.02616963
CT779	-	hypothetical protein	0.000716955	0.0316283
CT782	<i>cysS</i>	cysteinyl-tRNA synthetase	0.001021935	0.03265889
		glycyl-tRNA synthetase	0.000495571	0.02616963
CT840	<i>mesJ</i>	PP-loop superfamily ATPase/tRNA(Ile)-lysidine synthase	0.001320635	0.03638337
CT841	<i>ftsH</i>	ATP-dependent zinc protease/Cell division protein	0.002214862	0.0877202
CT847	-	hypothetical protein	0.000284971	0.01805816
CT875	-	hypothetical protein	3.71E-06	0.001176546
CT033	<i>recD_I</i>	exodeoxyribonuclease V alpha chain	0.000709905	0.0316283
CT108	<i>ybgI</i>	Acr family transporter	0.00213236	0.05162556
CT112	<i>pepF</i>	oligoendopeptidase F	0.000180174	0.01427168
CT114	-	hypothetical protein	0.000802599	0.0316283
CT149	-	hydrolase	0.003421852	0.07388864
CT223	-	hypothetical protein	0.001141791	0.05168107
CT249	-	hypothetical protein	0.003250097	0.07212935
CT286	<i>clpC</i>	ATP-dependent ClpC protease	0.000932156	0.0316283
CT288	-	Hypothetical protein/candidate inclusion membrane protein	2.76E-05	0.005837499
CT289	-	hypothetical protein	0.000116624	0.01055754
CT301	<i>pknD</i>	serine/threonine-protein kinase	0.004700505	0.09629375
CT305	<i>atpI</i>	V-type ATP synthase subunit I	0.000281513	0.01805816
CT306	<i>atpD</i>	V-type ATP synthase subunit D	0.001136536	0.03354957
CT315	<i>rpoB</i>	DNA-directed RNA polymerase subunit beta	5.83E-05	0.006627397
CT317	<i>rplJ</i>	50S ribosomal protein L10	0.001714316	0.07242233
CT327	<i>trpC</i>	N-(5'-phosphoribosyl)anthranilate	~0.000000574	~0.000000000

CT329	<i>xseA</i>	exodeoxyribonuclease VII large subunit	4.88E-05	0.006627397
CT379	<i>hflX</i>	GTP binding protein	0.001448642	0.03857962
CT397	<i>vacB</i>	exoribonuclease II	0.004524844	0.09513453
CT477	<i>ada</i>	methylated-DNA protein - cysteine methyltransferase	0.000924583	0.0316283
CT478	<i>oppC_2</i>	oligonucleotide transport system permease	6.28E-05	0.006627397
CT479	<i>oppB_2</i>	oligopeptide permease	0.003219834	0.07212935
CT480	<i>oppA_4</i>	oligopeptide transport system, binding lipoprotein	0.000950099	0.0316283
CT500	<i>ndk</i>	nucleoside diphosphate kinase	0.00107037	0.03289113
CT551	<i>dacC</i>	D-alanyl-D-alanine carboxypeptidase	0.001074055	0.05168107
CT609	<i>rpoN</i>	RNA polymerase factor sigma-54	0.001811551	0.04522918